IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:	
Gunji et al.	Art Unit: 1656
Application No.: 10/716,480	Examiner: Robinson
Filing Date: November 20, 2003	Attorney Ref. No.: US-102
For: METHOD FOR PRODUCING L-AMINO ACID USING METHYLOTROPH	**VIA EFS-WEB**

BRIEF FOR APPELLANT

Mail Stop Appeal Brief - Patents
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

COMES NOW the Appellant to present this Brief in support of the appeal of the final rejection of Claims 2-4 and 6-7 in the above-captioned patent application. The Notice of Appeal and a Petition for a two-month extension of time were timely filed on October 24, 2005. A Brief was timely filed on December 15, 2005. This Brief is identical to the Brief filed on December 15, 2005, except for corrections to the headings, as required by the Notice of Non-Compliant Appeal Brief ("Notice") sent by the PTO on September 5, 2006. As a one-month period for response was set forth in the Notice, this Brief is timely filed.

It is not believed that extensions of time are required, beyond those that may otherwise be provided for in accompanying documents. If, however, additional extensions of time are necessary to prevent abandonment of this application or dismissal of this appeal, then such extensions of time are hereby petitioned under 37 C.F.R. § 1.136(a), and the Commissioner is hereby authorized to charge fees necessitated by this paper, and to credit all refunds and overpayments, to deposit account 50-2821.

For the following reasons, Appellant respectfully submits that the final rejection of each of Claims 2-4 and 6-7 in this application is in error, and therefore respectfully requests reversal of the rejections.

TABLE OF CONTENTS

I. Real Party in Interest

The real party in interest is Ajinomoto Co., Inc, a corporation of Japan.

II. Related Appeals and Interferences

There are no related appeals or interferences.

III. Status of Claims

Claims 2-4 and 6-9 are pending. Claims 1 and 5 have been cancelled. Claims 8 and 9 are withdrawn from consideration. No claims have been identified in the Final Rejection as being in condition for allowance. Claims 2-4 and 6-7 were finally rejected in the Final Rejection dated 23 May 2005, and are on appeal.

IV. Status of Amendments

All amendments to the claims have been entered.

V. Summary of Claimed Subject Matter

The present invention relates to an isolated DNA encoding a mutant LysE protein, wherein said mutant is selected from the group consisting of a protein comprising the amino acid sequence of SEQ ID NO: 2 except that the glycine residue at position 56 is replaced with another amino acid residue, and a protein comprising the amino acid sequence of SEQ ID NO: 2 except that

i) the glycine residue at position 56 of SEQ ID NO: 2 is replaced with another amino acid residue, and

ii) not more than 10 amino acid residues at positions other than the 56th residue are substituted, deleted, or inserted, wherein said mutant imparts resistance to S-(2-aminoethyl) cysteine when introduced into a methylotroph (see paragraphs [0009] and [0033] to [0038], for example).

The present invention also relates to the above-described DNA, wherein said DNA is selected from the group consisting of a DNA which has the nucleotide sequence of SEQ ID NO: 1, except that a mutation which results in replacement of the 56th glycine residue of the encoded protein with another amino acid residue; and a DNA which is

hybridizable with the nucleotide sequence of SEQ ID NO: 1 under stringent conditions comprising washing in 1xSSC and 0.1%SDS at 60°C (see paragraphs [0010] and [0040], for example).

The present invention also relates to the above-described DNA, wherein said glycine residue at position 56 is replaced with a serine residue (see paragraph [0011] and [0040], for example).

The present invention also relates to the above-described DNA, wherein said methylotroph is a bacterium belonging to the genus *Methylophilus* or *Methylobacillus* (see paragraph [0013], [0051], and [0052], for example).

The present invention also relates to a bacterium comprising the above-described DNA in an expressible form, wherein said bacterium belongs to the genus *Methylophilus* or *Methylobacillus,* and wherein said bacterium has L-lysine or L-arginine producing ability (see paragraph [0053], for example).

VI. Issues to be Reviewed on Appeal

A. Whether Claims 2-4 and 6-7 are unpatentable under 35 U.S.C. § 112, 1st paragraph, scope of enablement.

VII. Argument

In the Final Rejection dated 23 May 2005, beginning at page 6, Claims 2-4 and 6-7 were rejected under 35 U.S.C. § 112, 1st paragraph, because the specification, while being enabling for a DNA of SEQ ID NO. 1, in which a mutation results in glycine residue 56 being replaced by serine, allegedly does not reasonably provide enablement for the genus of any DNA that encodes a mutant LysE protein of a coryneform bacteria. For at least the following reason, this rejection is in error and should be reversed.

A. Legal Standard

A claimed invention is unpatentable due to a non-enabling disclosure if the specification fails to describe how to make and how to use the invention. 35 U.S.C. § 112, 1st paragraph. The test for this standard is whether one reasonably skilled in the art could make or use the invention from the disclosures in the patent coupled with

information known in the art, without undue experimentation. *United States v. Telectronics, Inc.*, 857 F.2d 778, 785 (Fed. Cir. 1988). The seminal case in determining if a claim meets this standard is *In re Wands*, 858 F.2d 731, 737 (Fed. Cir. 1988), which promulgated a series of factors, set forth throughout the prosecution (*see,* for example, the First Office Action of November 18, 2004, page 14) to be considered when determining whether there is sufficient evidence to support a determination that a disclosure does not satisfy the enablement requirement and whether any necessary experimentation is 'undue.'

B. The rejection of Claims 2-3 and 6-7 under 35 U.S.C. § 112, 1st paragraph, enablement, is in error

Claims 2-4 and 6-7 were rejected under section 112, 1st paragraph, as allegedly lacking enablement. The Examiner alleged in the First Office Action that it would require undue experiment to make "all, or a relevant portion of, the nucleotides and polynucleotides within the scope of the claims" (see Office Action of November 18, 2004, page 15). Since receiving this Office Action, appellants amended the claims to indicate that no more than 10 other amino acid positions in SEQ ID NO. 2 can be substituted, deleted, or inserted. In the Advisory Action of October 18, 2005, the Examiner alleges that "...there is no indicia as to what residues the 'not more than 10 amino acids modification' will comprise...", or whether such a sequence will retain function. The position set forth in the Office Actions appears to imply that only a claim directed to a DNA having an exact sequence, with no variation, will satisfy the enablement requirement. Appellants respectfully disagree for the following reasons.

Appellants assert that the claims are fully enabled by the specification, and although every mutation encompassed by the claims is not explicitly exemplified by the specification, one of ordinary skill in the art would be able to determine those mutations that fall within the scope of the claims via routine experimentation. The Office Action of November 18, 2004, page 14, quotes *Wands*, stating that "Enablement is not precluded by the necessity for some experimentation such as routine screening. However, the experimentation needed to practice the invention must not be undue experimentation. The key word is 'undue', not 'experimentation'." It is well established in the case law

that enablement "is not precluded even if some experimentation is necessary, although the amount of experimentation needed must not be unduly extensive." *Hybritech Inc. v. Monoclonal Antibodies, Inc.* 802 F.2d 1367 (Fed. Cir. 1987), *cert. denied*, 480 U.S. 947 (1987). Finally, inoperable embodiments are permitted, as long as one skilled in the art is not required to experiment unduly to practice the claimed invention. *Atlas Powder co. v. EI du Pont de Nemours & Co.*, 750 F.2d 1569 (Fed. Cir. 1984).

Appellants acknowledge that some experimentation will be necessary to determine variants of the DNA which encodes a protein having not more than 10 amino acid residues, at positions other than the 56th residue, substituted, deleted, or inserted; however, such experimentation is not undue but merely routine for the person of ordinary skill in the art. The skill in this art area is very high. Furthermore, the Examiner has even acknowledged that "the instant specification describes and enables means for identifying other mutant LysE encoding genes using *in vitro* mutation, introduction of the DNA into *Methylophilus methylotrophus,* and selection on S-(2aminoethyl)cyctein containing media, etc..." (see the First Office action of November 18, 2004, page 15). The claims recite a DNA encoding a protein whereby not more than 10 amino acids in SEQ ID No. 2 (other then the 56th residue, which is specifically claimed) are substituted, deleted, or inserted. SEQ ID No. 2 recites an amino acid sequence of 236 amino acids. If the maximum number of amino acids are "substituted, deleted or inserted" according to the claim language, the percent variation in the amino acid sequence is not more than 4.2%, or the most variant protein will be 95.8% identical to SEQ ID No. 2. Therefore, the changes that are permitted are few, making the experimentation minimal, and clearly not undue. Techniques for screening variants and their concomitant activity are well described in the specification.

Furthermore, in response to the Examiner's comments in the Final Rejection of May 23, 2005 (top of page 7) and in an informal telephone interview with the Examiner on September 1, 2005, additional data to further support the arguments made in the response of February 15, 2005 was submitted (see evidence appendix). Alignment data showing the similarity of the LysE protein of *Corynebacterium glutamicum* (SEQ ID NO: 2) with other diverse LysE proteins from other bacteria was submitted in order to demonstrate that one of ordinary skill in the art would be able to routinely determine

substitutions, deletions, or insertions that might be made in the protein of SEQ ID NO:2 without changing the ability to impart resistance to S-(2-aminoethyl) cysteine when introduced into said methylotroph. Each submission will be explained in turn, as these data clearly show that the experimentation required to practice the claimed invention is routine and within the skill of the ordinarily skilled art worker.

First, appellants submitted alignment data of the LysE protein of *Coynebacterium glutamicum* (SEQ ID NO:2) and the YggA protein of *E. coli* (Appendix B). The YggA protein is a putative amino acid transport protein which shares similarity with LysE protein of *Coynebacterium glutamicum*. It is noted that the YggA protein is registered as NP_417398 and defined as being a member of the "LysE family" in the protein database of NCBI, as shown in pages 2-3 Appendix B. The alignment data shows that the YggA protein has Gly at position 57, which is presumed to correspond to Gly at position 56 of the LysE protein. This data also shows which positions are conserved and which are not between these two proteins, which are from diverse bacteria, and therefore provides ample and sufficient guidance as to which positions might be tolerant to substitution, deletion, or insertion of amino acids while maintaining the claimed activity of imparting resistance to S-(2-aminoethyl) cysteine when introduced into a methylotroph.

Secondly, appellants submitted alignment data of the LysE protein of *Coynebacterium glutamicum* (SEQ ID NO:2) and *Corynebacterium diphtheriae*, which shows that Gly at position 56 is also conserved in the amino acid sequence of the LysE protein of *Corynebacterium diphtheriae* (page 4 of Appendix B). For the sequence information of the LysE protein of *Corynebacterium diphtheriae*, please refer to pages 5-6 of APPENDIX B. This data presents another example of an alignment of two lysine exporter proteins, and which shows positions which are conserved and which are not, and therefore further provides additional guidance as to which positions might be tolerant to substitution, deletion, or insertion of amino acids while maintaining the claimed activity of imparting resistance to S-(2-aminoethyl) cysteine when introduced into said methylotroph.

Thirdly, appellants submitted an alignment of the claimed lysE protein (SEQ ID NO: 2) with the lysE protein from *Corynebacterium efficiens* (see pages 7-9 of Appendix B). This data provides even further evidence of the sequence characteristics of another

lysE protein, and hence provides even further information to the skilled art worker as to which positions might be tolerant to substitution, deletion, or insertion of amino acids while maintaining the claimed activity of imparting resistance to S-(2-aminoethyl) cysteine when introduced into said methylotroph.

This alignment data between LysE depicted in SEQ ID NO: 2 and lysE transporter-type proteins from *E. coli, Corynebacterium diphtheriae*, and *Corynebacterium efficiens* clearly show that one of ordinary skill in the art would be enabled to practice the claimed invention without undue experimentation, since lysE transporter proteins from other bacteria, even one as diverse as *E. coli*, were known, and such sequence information clearly would enable the skilled art worker to make or allow for variations to the sequence of up to 10 amino acids different from the sequence shown in SEQ ID NO: 2 while maintaining the ability to impart resistance to S-(2-aminoethyl) cysteine when introduced into said methylotroph.

In response to the submission of this wealth of information, the Advisory Action of October 18, 2005 entirely mischaracterized the data. For example, the Advisory Action stated:

> The alignments provided by applicant exemplify that the glycine at position 56 is conserved (see page 6 of the response, line 7), however, there is no indicia in the claims as to whether the "not more than 10 amino acids modification" will comprise, nor any indicia as to whether the sequence can tolerate any of the 20 naturally occurring amino acids or any non-naturally occurring amino acid substitution or insertion in to the claims SEQ ID NO:2.....Further, there are no indicia as to whether deletion of 10 residues in the sequence anywhere in the sequence other than at position 56 will retain function.

(See Advisory Action, page 5, underlining added for emphasis). In this passage, the benefit of the alignment data is only addressed in reference to the change at position 56. Subsequently in the passage, the Examiner's statement that there is "no indicia in the claims" of what the "not more than 10 amino acids" will comprise is misguided since it is not in the claims that said 'indicia' is found, but in the submitted alignment data. The Examiner does not reference, or even address, the alignment data. It is the alignment data that demonstrates that the specification adequately teaches and guides the skilled art worker as to which substitutions/deletions/insertions can be tolerated in the sequence

within the scope of the claims, that is, not more than 10 amino acids, or within 95.8% homology. In fact, the above phrase in the Advisory Action, and it is in the Advisory Action that the Examiner first evaluates the alignment data, clearly indicates that the data was not evaluated for its teachings relative to the enablement of the scope of the claims.

There are many factors that must be considered when evaluating the enablement of claim scope. Obviously, one must look at the support provided in the specification; however, one must also look at the state of the art at the time of the invention. The information about the LysE sequence from other bacteria, even those as diverse as *E. coli,* was known in the art. Knowledge of these sequences provides a wealth of structure-function relationship information, and combined with the information provided in the specification clearly provides sufficient structure-function information to allow one of skill in the art to determine other mutational species of these proteins which will retain the claimed function, particularly when the variance permitted by the claim is so small. Appellants assert that sufficient guidance has been provided, and combined with the general state of the art, in part demonstrated by the alignment data of record, one skilled in the art would be able to choose and determine through routine experimentation which mutants would possess the claimed activity.

For at least the foregoing reasons, Appellant respectfully submits that Claims 2-4 and 6-7 fully comply with 35 U.S.C. § 112, first paragraph, and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 112.

C. Claims 2-4 and 6-7 are patentable and fully meet the enablement requirement of 35 U.S.C. §112, 1st paragraph

For at least the reasons presented herein, each of the subject matters of Claims 2-4 and 6-7, taken as a whole, are patentable and meet the enablement requirement of 35 U.S.C. §112, 1st paragraph. Accordingly, the rejection of each of Claims 2-4 and 6-7 under section 112, 1st paragraph is reversible error.

VIII. Conclusion

For at least the foregoing reasons, Appellant respectfully submits that the subject matters of Claims 2-4 and 6-7, each taken as a whole, are patentable. Accordingly,

Appellant respectfully requests reversal of the rejections of Claims 2-4 and 6-7 under section 112, 1st paragraph.

Respectfully submitted,

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Date: September 7, 2006

APPENDIX A: CLAIMS ON APPEAL

2. An isolated DNA encoding a mutant LysE protein, wherein said mutant is selected from the group consisting of:

A) a protein comprising the amino acid sequence of SEQ ID NO: 2 except that the glycine residue at position 56 is replaced with another amino acid residue, and

B) a protein comprising the amino acid sequence of SEQ ID NO: 2 except that

i) the glycine residue at position 56 of SEQ ID NO: 2 is replaced with another amino acid residue, and

ii) not more than 10 amino acid residues at positions other than the 56th residue are substituted, deleted, or inserted, wherein said mutant imparts resistance to S-(2-aminoethyl) cysteine when introduced into a methylotroph.

3. The DNA of claim 2, wherein said DNA is selected from the group consisting of:

A) a DNA which has the nucleotide sequence of SEQ ID NO: 1, except that a mutation which results in replacement of the 56th glycine residue of the encoded protein with another amino acid residue; and

B) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 1 under stringent conditions comprising washing in 1xSSC and 0.1%SDS at 60°C.

4. The DNA of claim 2, wherein said glycine residue at position 56 is replaced with a serine residue.

6. The DNA of claim2, wherein said methylotroph is a bacterium belonging to the genus *Methylophilus* or *Methylobacillus*.

7. A bacterium comprising the DNA of claim 2 in an expressible form, wherein said bacterium belongs to the genus *Methylophilus* or *Methylobacillus,* and wherein said bacterium has L-lysine or L-arginine producing ability.

APPENDIX B: EVIDENCE

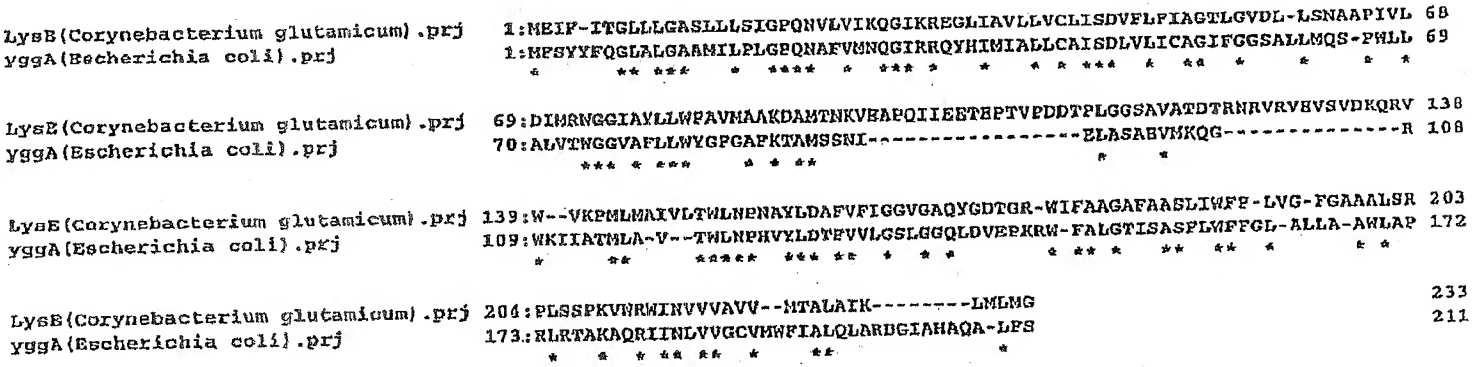
See attached.

APPENDIX C: RELATED PROCEEDINGS

None.

Sequence similarity between the LysE protein from *Corynebacterium glutamicum* and the YggA protein from *Escherichia coli*

Glycine residue



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VERSION     NP_417398.1  GI:16130824
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SOURCE      Escherichia coli K12
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REFERENCE   1  (residues 1 to 211)
  AUTHORS   Aleshin,V.V., Zakataeva,N.P. and Livshits,V.A.
  TITLE     A new family of amino-acid-efflux proteins
  JOURNAL   Trends Biochem. Sci. 24 (4), 133-135 (1999)
   PUBMED   10322417
REFERENCE   2  (residues 1 to 211)
  AUTHORS   Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V.,
            Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F.,
            Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J.,
            Mau,B. and Shao,Y.
  TITLE     The complete genome sequence of Escherichia coli K-12
  JOURNAL   Science 277 (5331), 1453-1474 (1997)
   PUBMED   9278503
REFERENCE   3  (residues 1 to 211)
  AUTHORS   Arnaud,M., Berlyn,M.K.B., Blattner,F.R., Galperin,M.Y.,
            Glasner,J.D., Horiuchi,T., Kosuge,T., Mori,H., Perna,N.T.,
            Plunkett,G. III, Riley,M., Rudd,K.E., Serres,M.H., Thomas,G.H. and
            Wanner,B.L.
  TITLE     Workshop on Annotation of Escherichia coli K-12
  JOURNAL   Unpublished
  REMARK    Woods Hole, Mass., on 14-18 November 2003 (sequence corrections)
REFERENCE   4  (residues 1 to 211)
  AUTHORS   Glasner,J.D., Perna,N.T., Plunkett,G. III, Anderson,B.D.,
            Bockhorst,J., Hu,J.C., Riley,M., Rudd,K.E. and Serres,M.H.
  TITLE     ASAP: Escherichia coli K-12 strain MG1655 version m56
  JOURNAL   Unpublished
  REMARK    ASAP download 10 June 2004 (annotation updates)
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  AUTHORS   Hayashi,K., Morooka,N., Mori,H. and Horiuchi,T.
  TITLE     A more accurate sequence comparison between genomes of Escherichia
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  JOURNAL   Unpublished
  REMARK    GenBank accessions AG613214 to AG613378 (sequence corrections)
REFERENCE   6  (residues 1 to 211)
  AUTHORS   Perna,N.T.
  TITLE     Escherichia coli K-12 MG1655 yqiK-rfaE intergenic region, genomic
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  CONSRTM    NCBI Genome Project
  TITLE      Direct Submission
  JOURNAL    Submitted (10-SEP-2004) National Center for Biotechnology
             Information, NIH, Bethesda, MD 20894, USA
REFERENCE    8  (residues 1 to 211)
  AUTHORS    Blattner,F.R. and Plunkett,G. III.
  TITLE      Direct Submission
  JOURNAL    Submitted (10-JUN-2004) Laboratory of Genetics, University of
             Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
  REMARK     Sequence update by submitter
REFERENCE    9  (residues 1 to 211)
  AUTHORS    Plunkett,G. III.
  TITLE      Direct Submission
  JOURNAL    Submitted (13-OCT-1998) Laboratory of Genetics, University of
             Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
REFERENCE    10 (residues 1 to 211)
  AUTHORS    Blattner,F.R. and Plunkett,G. III.
  TITLE      Direct Submission
  JOURNAL    Submitted (02-SEP-1997) Laboratory of Genetics, University of
             Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
REFERENCE    11 (residues 1 to 211)
  AUTHORS    Blattner,F.R. and Plunkett,G. III.
  TITLE      Direct Submission
  JOURNAL    Submitted (16-JAN-1997) Laboratory of Genetics, University of
             Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
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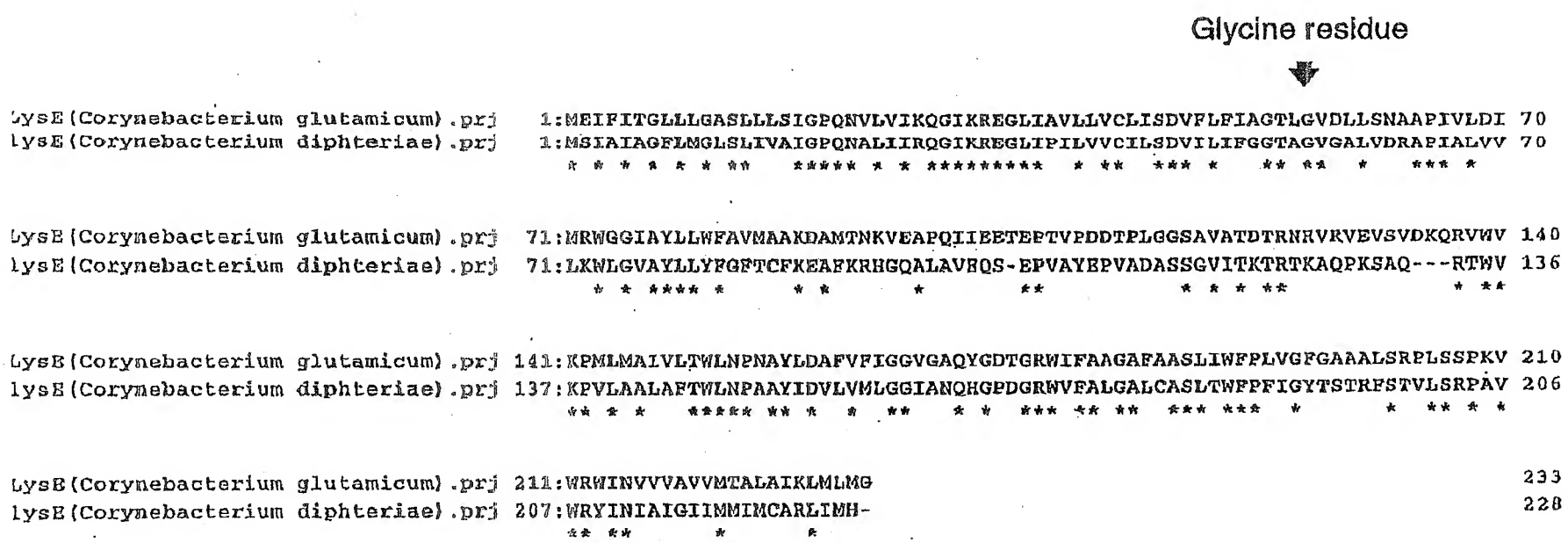
Sequence similarity between lysine exporter proteins from *Corynebacterium glutamicum* and *Corynebacterium diphtheriae*



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            Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE   1  (residues 1 to 228)
  AUTHORS   Cerdeno-Tarraga,A.M., Efstratiou,A., Dover,L.G., Holden,M.T.G.,
            Pallen,M., Bentley,S.D., Besra,G.S., Churcher,C., James,K.D., De
            Zoysa,A., Chillingworth,T., Cronin,A., Dowd,L., Feltwell,T.,
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            Whitehead,S. and Barrell B.G. Parkhill,J.
  TITLE     The complete genome sequence and analysis of Corynebacterium
            diphtheriae NCTC13129
  JOURNAL   Nucleic Acids Res. 31 (22), 6516-6523 (2003)
   PUBMED   14602910
REFERENCE   2  (residues 1 to 228)
  AUTHORS   Cerdeno-Tarraga,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-OCT-2003) Cerdeno-Tarraga A.M., submitted on behalf
            of the Pathogen Sequencing Unit, Sanger Institute, Wellcome Trust
            Genome Campus, Hinxton, Cambridge CB10 1SA E-mail:
            amct@sanger.ac.uk
REFERENCE   3  (residues 1 to 228)
  AUTHORS   .
  CONSRTM   NCBI Genome Project
  TITLE     Direct Submission
  JOURNAL   Submitted (08-APR-2002) National Center for Biotechnology
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Table 1

Sequence similarity of lysine exporter proteins from *Corynebacterium glutamicum* and *Corynebacterium efficiens*

Gly 56

```
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LysE(Corynebacterium glutamicum).prj   71:MRWGGIAYLLWFAVMAAKDAMTNKVEAPQIIEETEPTVPDDTPLGGSAVATDTRNRVRVEVSVDKQRVWV 140
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lysE(Corynebacterium efficiens).prj    136:RPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGETGRWIFAAGAFAASLVWFPLVGYGAAALSRPLSSPRV 205
LysE(Corynebacterium glutamicum).prj   141:KPMLMAIVLTWLNPNAYLDAFVFIGGVGAQYGDTGRWIFAAGAFAASLIWFPLVGFGAAALSRPLSSPKV 210
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lysE(Corynebacterium efficiens).prj    206:WRWINIGVAVVLTGLAVKLILMG 228
LysE(Corynebacterium glutamicum).prj   211:WRWINVVVAVVMTALAIKLMLMG 233
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DEFINITION  lysine exporter protein [Corynebacterium efficiens YS-314].
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VERSION     NP_737967.1  GI:25027913
DBSOURCE    REFSEQ: accession NC_004369.1
KEYWORDS    .
SOURCE      Corynebacterium efficiens YS-314
  ORGANISM  Corynebacterium efficiens YS-314
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE   1  (residues 1 to 235)
  AUTHORS   Nishio,Y., Nakamura,Y., Kawarabayasi,Y., Usuda,Y., Kimura,E.,
            Sugimoto,S., Matsui,K., Yamagishi,A., Kikuchi,H., Ikeo,K. and
            Gojobori,T.
  TITLE     Comparative complete genome sequence analysis of the amino acid
            replacements responsible for the thermostability of Corynebacterium
            efficiens
  JOURNAL   Genome Res. 13 (7), 1572-1579 (2003)
   PUBMED   12840036
REFERENCE   2  (residues 1 to 235)
  AUTHORS   .
  CONSRTM   NCBI Genome Project
  TITLE     Direct Submission
  JOURNAL   Submitted (15-NOV-2002) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
REFERENCE   3  (residues 1 to 235)
  AUTHORS   Kawarabayasi,Y., Yamazaki,J., Hino,Y., Kikuchi,H. and
            Director-General of Biotechnology Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAY-2002) Director-General of Biotechnology Center,
            National Institute of Technology and Evaluation, Biotechnology
            Center; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan
            (E-mail:bio@nite.go.jp, Tel:81-3-3481-1933, Fax:81-3-3481-8424)
COMMENT     PROVISIONAL REFSEQ: This record has not yet been subject to final
            NCBI review. The reference sequence was derived from BAC18167.
            Method: conceptual translation.
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                     /coded_by="complement(NC_004369.1:1422769..1423476)"
                     /note="similar to X96471-2|CAA65324.2| percent identity:
                     71 in 228 aa"
                     /transl_table=11
                     /db_xref="GeneID:1031976"
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       61 tlgvglisdt apiildilrw cgiayllwfa vmaardalra rtevtfvehs epvaaasasg
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```